SYNOPSIS OF P.G. RESEARCH PROJECT

ON

INHERITANCE OF SEX EXPRESSION IN CASTOR (*Ricinus communis* L.)

UNDER THE GUIDANCE OF

Dr. R. B. MADARIYA
RESEARCH SCIENTIST
MAIN OILSEEDS RESEARCH STATION
JUNAGADH AGRICULTURAL UNIVERSITY
JUNAGADH

SUBMITTED BY

KAPADIYA AVANI PRAVINBHAI

(Registration No.: 1010125008)

DEGREE FOR

Ph. D. (Agri.) Genetics and Plant Breeding

SUBMITTED TO

DIRECTOR OF RESEARCH AND DEAN
FACULTY OF P. G. STUDIES
JUNAGADH AGRICULTURAL UNIVERSITY
JUNAGADH - 362001

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE
JUNAGADH AGRICULTURAL UNIVERSITY
JUNAGADH - 362001

Date of Submission: / / 2026
Current Semester: Second

SYNOPSIS OF RESEARCH PROJECT

1.	**Name of the Student**	**:**	KAPADIYA AVANI PRAVINBHAI
2.	**Registration No.**	**:**	1010125008
3.	**Faculty**	**:**	Agriculture
4.	**Name of the Degree Submitted for**	**:**	Ph. D.
5.	**Major Subject**	**:**	Genetics and Plant Breeding
6.	**Minor Subject**	**:**	Molecular Biology and Biotechnology
7.	**Name of Major Guide**	**:**	Dr. R. B. Madariya Research Scientist Main Oilseeds Research Station Junagadh Agricultural University, Junagadh
8.	**Title of Research Project**	**:**	**INHERITANCE OF SEX EXPRESSION IN CASTOR (*Ricinus communis* L.)**

9. Introduction

Castor (*Ricinus communis* L.) is an important non-edible oilseed crop classified under *Euphorbiaceae* family and the tribe *Acalypheae*. It is the only cultivated species under the genus *Ricinus*. The trem *Ricinus* is a latin word which means ‘tick’. The plant is named probably because it seeds has markings and a dump at the end that resemble certain tick. The genus *Ricinus* is monotypic and *R. communis* is the only species with the most polymorphic forms known. Several of these forms were designated as species, *viz*., *R. communis*, *R. macrocarpus*, *R. microcarpus* (Weiss, 2000).

The crop is believed to have originated in tropical Africa, particularly in the Ethiopian region and subsequently spread to India and other tropical and subtropical regions of the world (Weiss, 2000; Anjani, 2012). India is now regarded as a secondary center of diversity for this crop due to the wide range of morpho-physiological and agronomic variations observed among the indigenous collections (Rao *et al*., 2011).

It is a cross-pollinated species with a chromosome number of 2n = 20 and exhibits monoecious flowering, where male and female flowers are arranged on the same inflorescence spike. Within the raceme, the upper 30-50 per cent portion consists of female flowers, while the lower 50-70 per cent portion contains male

flowers. *Ricinus communis* has been reported to be a secondary balanced polyploidy with basic chromosome number x = 5 likely derived from diploid ancestors (Singh, 1976). The wild species in the castor includes *Ricinus perciens, Ricinus chinesis* and *Ricinus maxicanus* (Kulkarni, 1959).

Castor is basically a long-day plant, but is adaptable with fewer yields to a wide range of photoperiod. It is short-lived small tree or shrub with soft wood and hollow stems which can grow to 5 m or more. The bark is smooth, greenish to reddish-brown in colour. Leaves are long-stalked, alternate, palmately and deeply lobed with serrated margins, dark green to reddish in appearance. The plant bears monoecious flowers arranged on upright spikes up to 40 cm long, with female flowers positioned at the upper portion of the spike appearing earlier than the male flowers located below. The fruits are round, deep red, prickly capsules borne in dense clusters, each containing three tick-like, brown to reddish-brown marbled seeds that are highly poisonous and rich in oil content (Rana *et al*., 2012).

India occupies the prime position in the global castor sector, contributing for > 80 per cent to the total world production and a major share of castor oil exports (FAOSTAT, 2023). During 2024-25, the area under castor cultivation in India was 8.28 lakh ha, with a production of 15.88 lakh tonnes and an average productivity of 1,918 kg/ha (Anonymous, 2024a). Among the Indian states, Gujarat ranks first in both area and production, followed by Rajasthan, Andhra Pradesh, Karnataka, Tamilnadu and Telangana. In Gujarat, castor occupied an area of 6.46 lakh ha during 2024-25, producing 14.03 lakh tonnes with a productivity of 2,170 kg/ha (Anonymous, 2024b). The semi-arid and arid tracts of North Gujarat; particularly the districts of Banaskantha, Mehsana, Patan, Sabarkantha and regions of Ahmedabad and Rajkot form the main castor-growing belt of the country (Patel *et al*., 2019). The success of castor cultivation in Gujarat is attributed to favourable climatic conditions, well-drained sandy loam soils and the extensive adoption of high-yielding hybrids developed by public and private sector breeding programmes (Anjani and Sridevi, 2016). It is predominantly cultivated across tropical, subtropical and warm temperate regions, owing to its adaptability to diverse climatic conditions (Weiss, 2000).

Among the nine major oilseed crops cultivated in India, castor (*Ricinus communis* L.) stands out as a unique non-edible oilseed crop with high industrial value. The seeds contain oil between 40 to 60 per cent, the highest among all cultivated oilseed crops that is rich in triglycerid, highly stable and variation in fatty

acids is very minimal making it the best raw industrial oil (Yadava *et al.,* 2012). Castor oil is unique because of its high content of ricinoleic acid (approximately 85-90%), a hydroxylated fatty acid that imparts special chemical and physical properties such as high viscosity, polarity and stability at both high and low temperatures (Mutlu and Meier, 2010). It is a versatile raw material for manufacturing lubricants, surfactants, coatings, cosmetics, nylon-11, polyurethane, pharmaceuticals and biodiesel (Muppala *et al.*, 2018). Castor oil is also used in the production of synthetic resins, greases, brake fluids and plasticizers. The residual castor cake, though toxic due to the presence of ricin and ricinine but it is rich in nitrogen, phosphorus and potassium and after detoxification, serves as valuable organic manure (Sailaja and Anjani, 2015). Thus, castor contributes significantly to both agricultural sustainability and industrial development.

Seed yield in castor is affected either directly or indirectly by several factors, among which sex expression particularly the proportion of pistillate whorls is considered highly important. Castor (*Ricinus communis* L.) shows sexual polymorphism that exhibits several sex forms such as monoecious, pistillate, pistillate with interspersed staminate flowers (ISF) and sex revertants. Under natural growing conditions, the majority of castor plants are monoecious. The expression of sex in castor is strongly influenced by environmental factors (Shifriss, 1960). Lower temperatures (below 30°C) and higher nutrient availability promote the development of female flowers, resulting in greater femaleness on the inflorescence. In contrast, higher temperatures (> 32°C), spikes of later order and low nutrient levels encourage the formation of male flowers (Lavanya, 2002).

According to Severino *et al*. (2012), pistillate lines in castor are classified into three major types: N, S and NES; as originally described by Shifriss (1960) and Ankineedu and Rao (1973). In the N-type, the presence of only female flowers is governed by a recessive gene (*ff*). In the S-type, the pistillate condition is determined by a polygenic system with dominant and epistatic effects. These plants initially produce only female flowers but may revert to producing male or mixed flowers at any stage of growth. The S-type pistillate lines are widely used in hybrid development programs due to their stable performance. In the NES-type, the plants possess the same recessive gene (*ff*) as in the N-type and initially produce only female flowers; however, when ambient temperatures exceed 31°C, a partial or complete sexual reversion to monoecy occurs.

The change in sex expression poses a significant constraint to the efficient production of hybrid castor seed. Therefore, maintaining stable pistillate expression under varying temperature conditions is a critical requirement for efficient and economically viable hybrid seed production. The success of hybrid breeding programs depends on the careful and rigorous evaluation of potential parental lines to identify the most suitable genotypes. This is particularly important because a parent's performance in isolation does not necessarily predict its performance in hybrid combinations.

Morphological traits in castor, such as stem color, leaf shape, bloom and capsule type exhibit considerable variation. These traits, along with sex expression are crucial for breeding programs aimed at hybrid development and enhancement of yield. Understanding the inheritance pattern of these characters is essential for selecting superior genotypes and enhancing castor productivity.

The success of any crop improvement programme is largely determined by the extent and efficient exploitation of genetic variability present in the germplasm. An assessment of genetic variability revealed the magnitude of variation among genotypes and helps to distinguish between heritable and environmental components of variation. The estimation of genetic parameters such as genotypic coefficient of variation, phenotypic coefficients of variation, genetic advance and heritability assists breeders in framing appropriate selection approaches for enhancing yield and its associated traits (Johnson *et al.*, 1955). Furthermore, understanding the association among different characters is crucial for identifying key traits contributing to yield and for implementing indirect selection approaches (Dewey and Lu, 1959).

The identification and selection of superior varieties, segregants, or populations are possible only when sufficient genetic variability exists within the gene pool. Therefore, understanding the magnitude and nature of variability in a crop species is of critical importance for effective plant breeding. The extent of variation in different characters can be compared using the coefficients of variation at both phenotypic as well as genotypic levels. In this regard, parameters like the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) provide essential information for designing efficient breeding strategies, particularly in crops like castor.

Since no single genotype or segregant can exhibit superior performance for all traits simultaneously, it is generally advisable to prioritize improvement of

individual traits based on their economic importance and breeding objectives. Estimates of heritability help quantify the proportion of total variation that is genetically determined, guiding breeders in the selection of elite genotypes from a diverse population. Despite this, it should be emphasized that a trait with high heritability does not always result in a high genetic advance, emphasizing the need for careful interpretation of these parameters in crop improvement programs.

The present investigation aimed to study and describe the genetic variability existing within the F_2 segregating population of castor through the use of morphological markers. The study further sought to precisely evaluate this variability for identifying promising segregants with superior yield potential and to elucidate the mode of inheritance governing sex expression in the F_2 generation.

10. Practical Utility of the Research Problem

Morphological traits possess certain economic advantages; for instance, castor varieties exhibiting a triple bloom nature show tolerance to jassids and drought. Such traits also serve as reliable diagnostic features to identify varieties, hybrids and their parental lines.

Castor stands out as highly polymorphic species and a brief understanding of its sex expression pattern provides important information on its breeding system, particularly for the effective exploitation of hybrid vigour.

Assessing genetic variability for seed yield and its component traits among different segregants provides a strong basis for the selection of superior lines aimed at yield enhancement and improvement of other agronomic traits.

Path coefficient analysis presents a more realistic understanding of the interrelationships among yield-contributing characters by partitioning the correlation coefficients into direct and indirect effects. Thus, correlation and path analyses together offer useful information for identifying key yield components, enabling breeders to effectively select and isolate superior accessions from the germplasm.

11. Objectives

Considering all these aspects, the present investigation entitled **"Inheritance of sex expression in castor (*Ricinus communis* L.)"** will be undertaken with the following specific objectives:

1. To study the inheritance pattern of different morphological traits and sex expression in F_2 population

2. To estimate the nature and magnitude of variability present in F_2 population with respect to yield and its contributing characters
3. To estimate genotypic and phenotypic correlation and direct and indirect effect of various yield attributing characters on yield through path analysis in F_2 population

12. Review of Literature

The available literature is briefly reviewed here under the following heads.

12.1 Inheritance of morphological traits and sex expression

Castor is a highly polymorphic species characterized by the presence of several series of determinate branches, each terminating in a raceme. The development of racemes along any given axis occurs sequentially, resulting in the simultaneous presence of racemes at different developmental stages on the same plant. This sequential pattern of raceme development plays an important role in influencing sex expression in castor.

The pistillate character in castor is greatly affected by modifier genes and environmental factors. Hence, sex tendency mainly depends on non-genetic variations governed by factors such as temperature, soil fertility, moisture availability, sowing time and the age of the plant (Shifriss, 1960). The pistillate trait is reported to be controlled by a single major recessive gene (*f*) (Classen and Hoffman, 1950; Zimmerman and Smith, 1966; Gopani *et al*., 1969). The interspersed staminate flowering (ISF) trait, on the other hand, is governed by two genes and its frequency is influenced by the dosage of the recessive alleles.

Ankineedu and Rao (1973) observed that in the “240 NES” type female, the occurrence of a few interspersed staminate flowers was not governed by raceme type but was influenced by temperature. Higher atmospheric temperatures (31-32 °C) encouraged the development of interspersed staminate flowers, whereas lower temperatures favored the expression of femaleness.

Patel *et al*. (1986) investigated the induction of male sex in pistillate lines of castor. The production of male flowers was induced in five pistillate lines by removing female flowers on primary, secondary and tertiary racemes. The induction of staminate flowers was lower at temperatures below 30 °C compared to temperatures above 32 °C. Variation among the lines suggested that sex expression is likely governed by more than one gene. The study further indicated that these lines could be maintained through selfing by removing female flowers from 50 % of the

racemes.

Solanki and Joshi (2001) utilized six parents, namely YP 1, MCP 2, RG 184, RG 125, RG 299 and 846 to produce five crosses: YP 1 × RG 299, YP 1 × RG 184, RG 184 × RG 299, MCP 2 × RG 125 and RG 125 × 846. Genetic analysis was carried out using six populations, *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2. The study revealed that green spike colour epistatic over sulphur white colour and trait being governed by a dominant inhibitory gene and another colour gene (sulphur white**)**. Inheritance of traits such as nature of internodes, presence of bloom and stem color were found to follow monogenic inheritance. Joint segregation analyses revealed that all studied traits segregated independently, with no evidence of linkage.

Lavanya and Gopinath (2008) studied inheritance pattern of morphological characters in four hybrids of pistillate × pistillate parental lines. Their finding revealed that stem colour was governed by single gene, with red stem colour being dominant over green stem colour. In the case of the DPC 13 × M 574 cross, green stem color and in the M 574 × DPC 11 cross, green coloration of petiole, capsules and spines exhibited a digenic epistatic ratio with respect to red stem color and red pigmentation of petiole, capsules and spines. The traits like plant type and bloom were found to be controlled by single genes, where normal plant type was dominant over dwarf type and presence of bloom was dominant over absence of bloom. Joint segegation analysis demonstrated that bloom, plant type and stem colour were assorted independently across all four crosses. Furthermore pistillate character was dominant over pistillate with interspersed staminate flowers (ISF) and was govern by one [P1], two [P1P2] or up to four genes [PIP2P3P4]. Joint segregation analysis revealed linkage between stem colour and dwarf plant type in the DPC 13 × DPC 11 as well as between the pistillate character [P1] and plant type [PtN] in the M 574 × DPC 11.

Shankar *et al*. (2010) carried out inheritance study to understand the genetics of stem colour, internode nature, leaf shape, bloom, spiny nature of the capsule and resistance to fusarium wilt by utilizing two crosses *viz*., YP 1 × PCS 142 (VP 1 - green stem, condensed internode, cup shaped leaf, triple bloom, spiny capsule and susceptible to wilt; PCS 142 - red stem, elongated internode, flat leaf, double bloom, nonspiny capsule and resistant to wilt) and M 574 × PCS 154 (M 574 - green stem, condensed internode, cup shaped leaf, triple bloom, spiny capsule and resistant to wilt; PCS 154 - red stem, elongated internode, flat leaf, zero bloom, non-spiny capsule and susceptible). Monogenic nature of inheritance was observed for stem

colour (red dominant over green), internode nature (elongated dominant over condensed), leaf shape (flat dominant over cup), bloom nature (triple dominant over double, triple partially dominant over zero) and spiny nature of the capsule (spininess is partially dominant over non-spininess). Joint segregation analysis of different pairs of trait revealed independent segregation for all the characters studied, with no evidence of linkage, except between leaf shape and internode length. All plants exhibiting condensed internodes possessed cup-shaped leaves, suggesting the presence of pleiotropic gene action or tight genetic linkage.

Rao *et al.* (2014) characterized fifty four genotypes based on their morphological characters as per DUS guidelines of castor *viz.*, stem colour, types of inter nodes on stem, plant branching pattern, petiole colour, bloom, type of inflorescence, lamina leaf colour, colour of stigma, spike shape, spike compactness, capsule type, seed colour. The germplasm has shown wide range of morphological variability for all the traits observed.

Patel *et al*. (2014) evaluated four segregating F_2 populations for various traits. Chi-square analysis of sex expression in castor revealed a good fit across all traits, environments and crosses to a 9:6:1 segregation ratio rather than the expected dihybrid ratio. This deviation indicated the involvement of polymeric gene interaction in the inheritance of this trait. Additional cycles of intermating in early segregating generations could be beneficial for exploiting such gene action. In both environments, sex expression was governed by polymeric gene action irrespective of the nature of the F_1 plants. However, the number of interspersed staminate flowers (ISF) was higher under irrigated conditions (E_2) compared to rainfed conditions, indicating that irrigation may be advantageous for maintaining plants with interspersed staminate flowers.

Patel *et al*. (2016) investigated the inheritance of four discrete morphological traits in castor *viz*., bloom, capsule spinyness, stem colour and leaf shape, using five genetically diverse parents (SKP 84, VP 1, GEETA, DCS 94 and GC 3) and three hybrid combinations (SKP 84 × DCS 94, VP 1 × DCS 94 and GEETA × GC 3) assessed across six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2). Their findings showed that each trait was governed by a single major gene. In the cross GEETA × GC 3, triple bloom was dominant over double bloom, evidenced by a 3:1 segregation in the F_2 and a 1:1 in the backcross. The same cross also revealed co-dominance for capsule

spinyness, where F_1 plants showed sparsely spiny capsules and the F_2 population fit a 1 spiny : 2 sparsely spiny : 1 non-spiny ratio. For stem colour, the cross SKP 84 × DCS 94 showed dominance of mahogany over green, confirmed by the classical 3:1 F_2 ratio and corresponding backcross results. Leaf shape also followed single-gene inheritance in both SKP 84 × DCS 94 and VP 1 × DCS 94, where flat leaves were dominant over cup-shaped leaves (3:1 in F_2 and 1:1 in BC populations).

Ramesh *et al*. (2017) studied the inheritance pattern of sex expression and morphological characters in castor using F_1 and F_2 generations developed from pistillate lines representing diverse genetic backgrounds, including S-type, NES and newly identified pistillate sources. The analysis of stem colour segregation showed that in four pistillate × monoecious crosses, the colour of stem was governed by a single dominant gene, with red dominant over green stem colour; however, one cross deviated from this pattern and exhibited a digenic epistatic ratio. Bloom colour displayed monogenic inheritance, with the presence of bloom dominant over its absence**.** Leaf shape, evaluated across three major crosses, was found to be controlled by two complementary genes, where the occurrence of either dominant allele resulted in semi-cup or flat leaves, while homozygous recessive genotype produced a cup-shaped leaf. Sex expression demonstrated a complex inheritance pattern, with monoecious sex expression dominant in certain crosses, while pistillate expression was dominant in others. Overall, the findings revealed that in castor sex expression is governed by a combination of genetic factors and environmental or physiological influences.

Panera *et al*. (2018) evaluated ten parental lines and six castor hybrids to investigate the inheritance pattern of morphological traits. Monogenic inheritance was observed for several characters, including colour of stem (mahogany dominance over green and red), internode nature (elongated dominant over condensed), leaf shape (flat dominant over cup), bloom nature (triple bloom dominant over double and single) and capsule spininess, where spininess showed partial dominance over non-spininess. The type of flowers on the primary raceme exhibited monoecious expression as dominant over interspersed and pistillate forms, while raceme shape was governed by conical dominance over cylindrical. For spike compactness, although monogenic control was suggested, the hierarchy of gene expression could not be clearly determined.

Chaudhari *et al*. (2019) characterized twenty-six castor genotypes for various morphological characters as per DUS guidelines, such as internode type, stem colour,

seed shape, plant type, leaf shape, bloom, spike type, inflorescence spike type, seed coat colour, branching habit, spike shape and capsule type. Traits such as triple bloom, medium plant stature, elongated internodes, conical spike shape, divergent branching habit and oval seed shape showed dominance. In contrast, traits including spike type, stem colour, capsule type, internode type and inflorescence spike type produced multiple classes of F_1 progenies across all crosses, suggesting the role of more than one gene and the occurrence of epistatic gene interactions.

Manjunatha *et al*. (2023) reported that morphological traits in castor, such as stem colour, leaf shape, branching pattern and inflorescence characters, generally follow mendelian inheritance, with stem colour governed by a single dominant gene (red over green). In contrast, sex expression exhibits complex inheritance, requiring coordinated gene action for pistillate and staminate flower development. The occurrence of interspersed staminate flowers (ISFs) is primarily temperature-dependent, while other environmental factors have minimal influence. Genes controlling ISF production are distinct from that regulating sex reversion and pistillate expression can remain stable under high temperatures, reflecting strong genetic control. Evaluation of six pistillate lines (DPC 22, IPC 30, IPC 31, DPC 9, SKP 84 and M 574) across four Indian environments showed that IPC-30 maintained stable pistillate expression with minimal ISFs, whereas DPC 22 and IPC 31 were relatively early flowering.

Deepika *et al*. (2025) examined the inheritance of morphological traits and sex expression in castor using eight crosses involving five pistillate lines (YRCP 1, YRCP 2, DPC 9, JP 65 and SKP 84) and three monoecious lines (YTP 1, TMV 5 and SKI 215). Their findings indicated that most morphological traits, particularly stem colour, are predominantly governed by monogenic inheritance, with red stem colour showing dominance over green and red × green crosses expressing mahogany colour because of the predominance of anthocyanin pigmentation. Spiny × non-spiny crosses exhibited intermediate spine development, suggesting partial dominance. With respect to sex expression, pistillate × monoecious (JP 65 × SKI 215) and monoecious × monoecious (YTP 1 × TMV 5) crosses produced monoecious progenies, confirming the recessive nature of pistillate sex expression, whereas several pistillate × pistillate crosses *viz*., DPC 9 × JP 65, YRCP 1 × DPC 9 and YRCP 2 × DPC 9 expressed stable pistillate sex in both primary and late-order spikes. In contrast, YRCP 2 × SKP 84 expressed pistillate sex only in the primary spike and reverted to monoecious nature

in subsequent spikes, indicating differential genetic regulation of sex expression. The occurrence of a 13:3 (monoecious : pistillate) segregation ratio in crosses like, YTP 1 × TMV 5, YRCP 2 × DPC 9, DPC 9 × JP 65 and YRCP 2 × SKP 84 indicates the involvement of inhibitory epistasis along with single-gene control of sex expression. Overall results indicated that inheritance of morphological traits and pistillate sex expression is controlled by a major gene system modified by epistatic interactions and other non-genetic factors.

12.2 Variability parameters

Assessment of genetic variability is a prereqirement for initiating suitable breeding procedures and for advancing subsequent generations in crop improvement programmes. The variation present in any population may be attributed to both genetic and environmental factors, Johansen (1909), who explain that the variation in a segregating population is due to both heritable (genetic) and non-heritable (environmental) factors and variation within pure line due to only environmental factors. Nilsson Ehle (1909) later confirmed Johanssen's findings and illustrated that continuous variation also confirms to Mendelian genetics.

Sevugaperumal *et al*. (2000) studied genetic variation in 36 castor genotypes and reported the single plant yield exhibited the highest GCV, succeeded by the number of spikes per plant and plant height. The difference between GCV and PCV was minimal for most traits, indicating lower influence of environment. Single plant yield, 100-seed weight, plant height, length of primary raceme and number of spikes per plant shown moderate to high heritability as well as genetic advance.

Lakshmamma *et al*. (2005) evaluated genetic variability in different 68 castor germplasm lines, including hybrids and cultivars. High genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were recorded for traits like, capsule weight per plant, number of capsules and plant height. Traits such as capsule weight, plant height, leaf area index and capsule number showed high heritability along with high genetic advance suggesting the preponderance of additive gene action. In contrast, stem girth, internodal length, seed yield and number of secondary and tertiary branches exhibited high heritability but low genetic advance, suggesting the influence of non-additive gene effects.

Sridhar *et al.* (2009) conducted an investigation to assess genetic variation in four F_2 populations of castor. The data were collected from one hundred random plants per replication for seven morphological characters *viz.*, plant height, effective

spike length, number of nodes up to primary raceme, primary spike length, 100-seed weight, number of capsules per primary raceme and seed yield per plant. Phenotypic coefficients of variation (PCV) were greater than the corresponding genotypic coefficients of variation for all the traits studied. High heritability coupled with high genetic advance as per cent of mean was exhibited by plant height followed by primary spike length indicating the operation of additive genetic action in these traits. 100-seed weight, number of nodes up to primary spike and seed yield per plant showed low to moderate heritability coupled with low to moderate genetic advance as per cent of mean, which suggests the presence of non-additive gene action in control of these characters.

Patel *et al*. (2010) evaluated genetic variability among 41 castor genotypes for nine quantitative traits. The maximum genotypic and phenotypic coefficients of variation were recorded for the number of capsules on the primary raceme, followed by plant height, number of effective branches per plant and seed yield per plant. Across all the traits, PCV values exceeded GCV values, suggesting the influence of environmental factors. High genetic variability along with high heritability and genetic advance for plant height, number of capsules on the primary raceme, number of effective branches per plant and seed yield per plant suggested that these characters can be effectively improved through direct selection.

Ahmed *et al*. (2012) studied variability and morphological characters in castor. The number of capsules on the main spike, number of spikes per plant and main spike length showing high heritability along with high genetic advance, indicating that additive gene action is predominant and seed yield improvement can be effectively achieved through selecting these traits. Additionally, 100-seed weight and spike length were also identified as important traits for enhancing seed yield.

Kote *et al*. (2013) evaluated genetic variability in castor for yield and its contributing traits and reported considerable amount of variability among all characters. The phenotypic coefficient of variation exceeded the genotypic coefficient of variation for all characters, indicating that environmental variance plays a significant role in the total variance. All characters exhibited high heritability except for oil content and L/B ratio, the traits showed high heritability coupled with high genetic advance, suggesting the predominant role of additive gene action and the effectiveness of direct selection for their improvement.

Alemaw *et al*. (2014) studied phenotypic variability in Ethiopian castor. In

all traits, a combined analysis of variance over locations revealed significant variation among accessions. In which 12 traits studied, the interaction between accessions and environment was significant. Highest values of GCV (genetic coefficient of variability) were observed for number of nodes per plant, number of capsules per plant, and 100 seed weight. They found overall the highest value of heritability, genetic coefficient of variation and genetic advance as per cent of mean for number of nodes per plant, number of capsules per plant and 100 seed weight.

Variability parameters were studied by Patel and Patel (2014) for seed yield and its component characters in castor. Seed yield at 120 days showed the greatest phenotypic coefficient of variation. At 120 days, seed yield displayed the highest genotypic coefficient of variation. With respect to heritability, the highest values were seen for number of nodes up to primary spike, plant height up to primary spike, number of capsules on primary spike and seed yield at 120 days after sowing. Seed yield at 210 days after sowing exhibited the highest genetic advance as a per cent of mean, followed by seed yield at 180 days after sowing, seed yield at 150 days after sowing, number of capsules on primary spike and seed yield at 120 days after sowing.

Chaudhari *et al.* (2016) conducted an investigation in 72 castor (*Ricinus communis* L.) genotypes. The genotypic and phenotypic coefficient of variation was high for effective spike per plant (GCV 31.92%, PCV 33.49%) followed by number of capsules per primary spike (GCV 25.07%, PCV 27.64%) and plant height up to primary raceme (GCV 23.53%, PCV 25.75%). High heritability with high genetic advance was recorded for effective spike per plant followed by effective primary spike length, plant height up to primary raceme, seed yield per plant, number of capsule per primary spike and number of node to primary raceme.

Movaliya *et al*. (2018) investigated variability in 64 castor genotypes. High genotypic and phenotypic coefficient values were recorded for the plant height up to the primary raceme, number of effective branches per plant, seed yield per plant and number of capsules on the primary raceme. Conversely, traits such as oil content, days to maturity of the main raceme, shelling outturn and days to 50 per cent flowering of the main raceme showed low GCV and PCV. Moderate levels of GCV and PCV were recorded for 100-seed weight, effective and total length of the main raceme and number of nodes up to the primary raceme. High heritability estimates were recorded for plant height up to the main raceme, number of effective branches per plant, days to 50 per cent flowering of the main raceme, effective length of the main raceme,

number of capsules on the main raceme, 100-seed weight and seed yield per plant. The highest genetic advance was obtained for seed yield per plant and plant height up to the main raceme, followed by moderate genetic advance for effective length of the main raceme and number of capsules on the main raceme, whereas the remaining traits exhibited low genetic advance, suggesting comparatively lower response to selection.

An experiment was carried out by Rukhsar *et al*. (2018) to determine the nature and extent of variability among castor genotypes for yield and its component characters. The study involved fifteen genotypes evaluated for variability, correlation, path coefficient analysis and genetic divergence across thirteen characters. The variability in oil content ranged from 46.75% to 51.71%. High genotypic and phenotypic coefficients of variation were found for the number of capsules on the main raceme.

Alhaji *et al.* (2019) conducted a study to assess genetic variability among ten castor genotypes in a randomized complete block design. The analysis of variance revealed that the presence of significant differences among genotypes for all the characters under study. High genotypic and phenotypic coefficients of variation were observed for days to 50% flowering (26.78%, 27.22%), effective racemes per plant (47.63%, 53.93%), number of capsules per raceme (22.30%, 27.77%) and effective length of raceme (22.59%, 29%), indicating substantial variability for these characters. High heritability coupled with high GAM (genetic advance as percentage of mean) were recorded for days to 50 per cent flowering, height at flowering, number of effective racemes per plant, length of effective spike, number of capsule per spike, height at maturity and 100 seeds weight.

Sowmya *et al*. (2019) evaluated 23 CRIDA genotypes of castor for seed yield and its components, *viz.*, number of branches, capsule number, number of nodes and capsule weight. Significant differences were observed for all the traits studied among all the genotypes. Capsule number, capsule weight and seed yield exhibited high heritability and genetic advance, indicating that selection based upon these traits would be effective in improving seed yield.

Yamanura and Kumar (2020) investigated genetic variability in castor using multivariate analysis involving 33 genotypes comprising 20 hybrids, 12 parents and a check (ICH 66). The results revealed a high degree of variability present among the genotypes. High heritability coupled with high combining ability was observed for

traits like, days to 50% flowering, plant height up to the primary raceme, days to maturity, number of nodes up to the primary spike, number of effective spikes per plant volume and seed weight, and seed yield, indicating the preponderance of additive gene action for these characters.

Sadaiah *et al*. (2021) evaluated 82 castor accessions using an augmented design to estimate genetic parameters such as phenotypic and genotypic coefficients of variation, heritability and genetic advance as per cent of mean. The results revealed low difference between phenotypic and genotypic coefficients of variation which indicated that minimal influence of environmental factors on trait expression. High heritability along with high genetic advance as per cent of mean was recorded for traits such as days to 50% flowering, days to maturity, plant height, number of nodes up to the primary spike, number of capsules per plant, 100-seed weight and seed yield per plant. This indicates the predominance of additive genetic action, suggesting that these traits can be effectively improved through phenotypic selection. In contrast, number of effective spikes per plant, primary spike length and effective spike length exhibited moderate heritability along with high genetic advance as per cent of mean, indicating a considerable influence of environmental factors on their inheritance.

Lavanya *et al*. (2022) studied genetic variability for seed yield and yield-attributing traits in a segregating population developed by crossing two pistillate castor lines, IPC 23 and IPC 21. The difference between phenotypic and genotypic coefficients of variation was low to moderate for number of effective spikes per plant, number of nodes up to the primary spike, plant height, total spike length and effective spike length, indicating that phenotypic selection can effectively applied for yield improvement. High estimates of heritability together with high genetic advance as per cent of mean (GAM) were noted for plant height and total and effective primary spike length suggesting the predominance of additive gene action, indicating that these traits can be directly selected for yield improvement. In contrast, low heritability with high GAM for seed yield per plant indicated the influence of non-additive gene action on this trait.

Reddy *et al*. (2022) evaluated fifty castor lines derived from a random mating gene pool and selfed up to homozygosity, along with two checks (Pragathi and DPC 9), for ten phenotypic traits. The genotypic and phenotypic coefficients of variation (GCV and PCV) indicated broad variability for all the traits except for days to 50% flowering and days to maturity. Among all the traits, plant height, number of

nodes to primary raceme, effective primary raceme length, primary raceme length, number of effective racemes per plant, 100-seed weight, number of capsules in the primary raceme and seed yield showed high heritability along with high genetic advance as per cent of mean, that suggesting their inheritance is predominantly governed by additive genetic action with minimal environmental influence, making them suitable for direct selection. Days to 50% flowering recorded high heritability but moderate genetic advance, indicating the involvement of both additive and non-additive gene action and a considerable environmental effect. On the other hand, days to maturity displayed high heritability but low genetic advance, implying predominance of non-additive gene action and significant environmental influence on its expression.

Deepak *et al*. (2024) evaluated genetic diversity in 15 male (monoecious) and 15 female (pistillate) advanced castor breeding lines. For all traits, the genotypic coefficient of variation (GCV) was lower as compared to the phenotypic coefficient of variation (PCV), indicating minimal environmental influence and suggesting that phenotypic selection could be effectively employed for improvement. High heritability were observed for days to 50% flowering, days to 50% maturity, number of nodes, total length of primary spikes and effective length of primary spikes, reflecting additive gene action and the scope for improvement through direct selection. Moderate heritability was reported for hundred-seed weight and total seed yield per plant, signifying that these traits are influenced by both genetic and environmental factors.

Yamanura *et al*. (2024) evaluated 40 castor genotypes to explore the genetic variability of major yield-related traits. Genetic estimates revealed narrow difference between genotypic and phenotypic coefficients of variation for traits such as seed yield, plant height, 100-seed weight, effective primary spike length and number of capsules on primary spikes, indicating minimal influence of environmental on expression of these traits. They reported most quantitative predominance of additive gene action which makes them suitable for direct selection.

In order to estimate genetic variability, Bhat *et al*. (2025) evaluated fifty advanced castor breeding lines along with two check varieties PCS 262 and DPC 9 with augmented randomized complete block design. High genotypic coefficient of variation (GCV) was recorded for effective length of primary spike (21.57), seed yield per plot (22.06), number of capsules per primary spike (27.25) and number of

effective spikes per plant (28.61), indicating the presence of substantial amount genetic variability and greater possibility of improvement through selection. High GAM (genetic advance as per cent of mean) was recorded for plant height (30.20%), 100-seed weight (31.90%), total length of primary spike (35.10%), effective length of primary spike (40.20%), seed yield per plot (42.30%), number of capsules per primary spike (47.90%) and number of effective spikes per plant (56.4%). Further, high GCV along with high heritability was noted for seed yield per plot (22.06% and 86.44%, respectively), number of capsules per primary spike (27.25% and 81.56% respectively) and primary spike length (18.53% and 96.93% respectively).

12.3 Correlation and path analysis

The concept of correlation was given by Galton (1889) and later it was extended by Fisher (1918). Path analysis was initially suggested by Wright (1921) in animal breeding but was applied for the first time for crop plants by Dewey and Lu (1959). A brief summary of the experimental work pertaining to correlation and path coefficient analysis in castor (*Ricinus communis* L.) is presented below.

Gogoi *et al.* (2009) evaluated twenty-two indigenous castor bean genotypes to assess genotypic and phenotypic correlations along with path coefficient analysis. The findings indicated that leaf yield per plant showing significant positive correlations with leaf area, leaf moisture content, raceme length, number of capsules per raceme and hundred-seed weight. Most quantitative traits exhibited significant positive correlation coefficients at genotypic as well as phenotypic levels. Leaf yield exhibited significant positive associations with all studied traits, except for the relationship between leaf moisture content and hundred-seed weight. Path coefficient analysis at the genotypic level indicated that seed weight exerted the maximum direct effect on leaf yield, followed by capsules per raceme and leaf area. Seed weight also demonstrated substantial positive indirect effects via leaf moisture content, leaf area and capsules per raceme. Consequently, selection based on seed weight, capsules per raceme, leaf area and leaf moisture content was identified as crucial for improving leaf yield. The study further highlighted the potential for developing castor bean genotypes with enhanced leaf and seed productivity.

Dhedhi *et al*. (2010) carried out correlation and path coefficient analysis in 29 genotypes. Correlation study revealed that seed yield exhibited positive and significant association at genotypic and phenotypic level with leaf length, capsule length, length of primary spike and 100-seed weight. Path coefficient analysis

indicated that leaf length, length of primary spike, number of nodes and days to 50 % flowering were the key traits exhibiting large direct effects on seed yield per plant.

Correlation studies conducted by Patel *et al.* (2011) on eleven castor inbreds suggested that days to 50 per cent flowering had a positive and significant correlation with days to 80 per cent maturity, oil content, wilt incidence and stem length, whereas it was negatively correlated with hundred seed weight and number of capsules on the primary spike. Path coefficient analysis showed that seed yield per plant had a positive and direct effect from number of branches per plant, followed by effective raceme length (cm) and number of capsules on the primary spike.

Ahmed *et al.* (2012) evaluated correlations and path coefficient analysis using morphological traits in the M_4 and M_5 generations of gamma-irradiated castor. Capsule yield per plant showed a significant and positive correlation with seed yield. 100-seed weight exhibited positive but non-significant phenotypic correlation and a significant genotypic correlation with seed yield. Capsule yield per plant also exerted a high direct effect on seed yield, coupled with a high positive and significant genotypic correlation.

Chaitanya *et al*. (2013) carried out studies on character associations and path coefficient analysis involving thirty castor genotypes. Their findings showed that seed yield per plant showed positive and significant associated with 100-seed weight, oil yield per plant, effective length of the main spike, oil content and number of spikes per plant. Path analysis indicated that oil yield per plant, 100-seed weight, number of capsules on the main spike, number of nodes up to the main spike and days to 50 per cent flowering were the major direct contributors to seed yield in castor.

Tewari and Mishra (2013) conducted correlation and path coefficient analysis in 30 castor accessions. The results demonstrated that genotypic correlations generally showed more significant differences among the pairs of traits than the phenotypic correlations. Seed yield per plant had highest positive and significant association with number of effective spikes per plant and number of capsules on the primary raceme at genotypic as well as phenotypic levels. Path coefficient analysis further revealed that number of capsules on the primary raceme had a positive and highly significant direct effect on the seed yield per plant at the phenotypic level.

Sowmya *et al*. (2015) evaluated the correlation between seed yield and its contributing characters in castor (*Ricinus communis* L.) germplasm under rainfed conditions. Correlation studies revealed that all yield-related characters shown highly

significant and positive associations with seed yield. As seed yield is a complex trait governed by the combined expression of several component characters, the study suggested that direct selection of these traits could be effectively employed to enhance seed yield.

Genetic correlation analysis of seed yield were carried out by Dapke *et al.* (2016) using sixty-one castor genotypes comprising 44 hybrids (including two checks) and 17 parental lines. The experiment was performed in a randomized block design with three replications at the College Farm, Navsari Agricultural University, Navsari, Gujarat, during *rabi* 2014. Correlation analysis indicated that seed yield per plant exhibited significant and positive correlation at genotypic and phenotypic level with plant height up to primary spike, total length of primary spike, length of the capsule-bearing region of the primary spike, number of effective branches per plant, number of capsules on the primary spike and oil content, indicating their importance as yield-contributing traits. Path coefficient analysis further showed that number of capsules on the primary spike (0.609), number of effective branches per plant (0.429) and oil content (0.157) exerted high direct effects on seed yield per plant.

Patel and Nakarani (2016) conducted studies on character association and path coefficient analysis in castor. Total seed yield per plant exhibited significant positive correlations with seed yield recorded at 120, 150 and 180 days after sowing, total and effective length of the primary spike, 100-capsule weight, 100-seed weight, shelling percentage and oil content. Seed yield showed significant and negative correlation with number of nodes up to the primary spike and seed specific gravity. Path coefficient analysis indicated that seed yield at 120 and 180 days after sowing, effective length of the primary spike and seed specific gravity exerted high direct effects in a positive and desirable direction on total seed yield. In contrast, number of nodes up to the primary spike and total length of the primary spike exhibited high direct effects in the negative direction. Despite this, their significant association with total seed yield suggested the presence of true and perfect of perfect correlation between association between these traits.

Mullualem *et al*. (2017) investigated the association between seed yield and yield-related components in castor (*Ricinus communis* L.) using 48 accessions. The results revealed that seed yield has significant and positive phenotypic and genotypic associations with number of capsules per plant, number of seeds per plant, internode length, number of primary branches per plant, number of secondary branches per

plant and number of inflorescences per plant. Oil content has also positive and significant genotypic correlation with seed yield. Seed yield had high and positive correlated with number of primary branches per plant (r = 0.488), number of seeds per plant (r = 0.413), number of secondary branches per plant (r = 0.376) and internode length (r = 0.279). It showed weak but positive correlations with number of capsules per plant (r = 0.318) and number of inflorescences per plant (r = 0.180).

Movaliya *et al.* (2018) conducted a trial to assess variability and correlation for seed yield and its attributing traits with a set of 64 genotypes of castor (*Ricinus communis* L.). The 12 quantitative characters were studied *viz*., days to 50% flowering of main raceme, number of nodes up to main raceme, days to maturity of main raceme, effective length of main raceme, number of capsules on main raceme, plant height up to main raceme, total length of main raceme, number of effective branches per plant, seed yield per plant, 100-seed weight, oil content and shelling out turn. In the present experiment, seed yield per plant exhibited a highly significant and positive association with total length of main raceme, effective length of main raceme and number of capsules on main raceme at both genotypic and phenotypic levels. Whereas oil content and days to maturity of the main raceme exhibited significant positive correlations with seed yield per plant only at the genotypic level.

Rukhsar *et al.* (2018) conducted an experiment to estimate the nature and extent of genetic variability in castor genotypes in relation to seed yield and its contributing traits. Seed yield per plant showed a positive association with number of nodes up to the primary raceme and total length of the primary raceme, indicating that these traits could be directly exploited for improving seed yield. Days to maturity exhibited a negative correlation with seed yield, suggesting that medium to long duration genotypes may be desirable for enhancing yield in castor. Path coefficient analysis further revealed that total length of the primary raceme (0.62) showed highest positive direct effect on seed yield per plant, followed by number of nodes up to the primary raceme (0.44).

Venkatachalam *et al.* (2019) reported that genotypic and phenotypic correlations were of comparable magnitude, with genotypic correlations being higher than phenotypic correlations in most cases. The highest significant genotypic correlation was found between seed yield per plant and total number of racemes per plant (0.390). Path coefficient analysis indicated that total number of racemes per plant showed the highest positive total indirect effect (0.386) through days to

flowering, days to maturity and primary raceme length. Days to flowering and days to maturity exhibited negative total indirect effects; however, these effects were very low and negligible.

The research was undertaken by Yamanura and Kumar (2020) to investigate genetic variability in castor through multivariate analysis. Correlation analysis revealed a strong and positive association of seed yield with oil content (0.717), 100-seed weight (0.679), 100-volume weight (0.527), number of capsules per primary raceme (0.443), effective length of the primary spike (0.245), total length of the primary spike (0.216) and number of effective spikes per plant (0.012). The residual effects were 0.63 and 0.73 at the genotypic and phenotypic levels, respectively. These results indicated that, apart from the yield-contributing traits identified, other extraneous traits also influenced seed yield in castor.

Sadaiah *et al.* (2021) evaluated eighty diverse castor germplasm lines using an augmented design. Correlation analysis revealed that plant height had a significant positive association with number of nodes, primary spike length, effective primary spike length, number of capsules per primary spike and total yield per plant. Number of nodes up to the primary spike showed significant positive correlations with primary spike length, effective primary spike length, number of effective spikes per plant, number of capsules per primary spike, total yield per plant and 100-seed weight. Number of capsules per primary spike and 100-seed weight also exhibited significant positive correlations with total yield per plant.

Deepika *et al.* (2022) evaluated 208 castor genotypes for morphological diversity using an augmented block design. All yield-attributing traits showed significant positive correlations with seed yield, with capsule weight recording the highest association. Path coefficient analysis revealed a high coefficient of determination ($R^2 = 0.8834$) and low residual effect (0.3415). Effective spike length and capsule weight exhibited high positive direct effects on seed yield, while 100-seed weight and primary spike length showed high negative direct effects, indicating the predominance of indirect effects. Primary spike length and effective spike length were identified as major contributors based on eigenvalue analysis.

Correlation studies were conducted by Sadaiah *et al*. (2023). The results indicated that, seed yield has significant positive association with primary spike length, effective primary spike length and number capsules per primary spike whereas days to 50 per cent flowering has significant and positive association with number of

nodes to primary spike. Number of nodes also shown positive significant association with plant height, primary spike length and effective primary spike length. Primary spike length and effective primary spike length were positively correlated with each other and with number of capsules per primary spike and 100-seed weight.

Yamanura *et al.* (2024) evaluated forty castor genotypes for trait association and path coefficient analysis. The results revealed that seed yield per plant has positive association with total length of primary spike (0.0765), effective length of primary spike (0.0425), oil content (0.289) and 100-seed weight (0.1775), indicating that selection for these traits would result in higher seed yield per plant. While, days to 50 per cent flowering of the primary spike, number of nodes to the primary spike and number of effective spikes per plant exhibited negative correlations with seed yield per plant. The results of path coefficient analysis revealed that total length of primary spike (1.8104), days to maturity of primary spike (0.355), oil content (0.3235) and 100-seed weight (0.1132) exerted the maximum positive direct effects on seed yield per plant. Therefore, these traits can be directly exploited for the enhancement of seed yield through the selection of superior genotypes.

Bhat *et al.* (2025) conducted an experiment to evaluate fifty advanced castor breeding lines. Correlation analysis revealed that, days to 50 per cent flowering was positively associated with plant height and number of nodes up to the primary spike. Days to maturity of the primary spike were positively correlative with plant height, effective spike length and number of nodes. Seed yield per plot showed strong positive associations with number of capsules, hundred-seed weight, total and effective spike length and oil content, while earlier flowering contributed to higher seed yield. According to the findings, traits such as primary spike length, effective spike length and hundred-seed weight should be prioritized to improve seed yield and oil content.

13. Materials and Methods

The experimental material consisted of parents, F_1 and F_2 of four crosses *viz.*, SKP 84 × JI 546, ANDCP-16-1 × JI 546, JP 105 × JI 546 and JP 107 × JI 546. The parents and F_1 were procured from Main Oilseeds Research Station, J.A.U., Junagadh. F_1 will be grown and selfed to produce F_2 generation.

13.1 Experimental details

i.	**Location**	**:**	Main Oilseeds Research Station J.A.U, Junagadh
	Year and season of experiment		
ii.	a) Development of F_2 population b) For evaluation of experimental material	**:**	*Kharif*-2025-26 *Kharif*-2026-27
iii.	**Experimental design**	**:**	RBD (Randomized Block Design)
iv.	**Number of replications**	**:**	3 (Three)
v.	**Spacing**	**:**	120 x 60 cm
vi.	**Treatment details**	**:**	1) Five parents 2) Four F_1 combinations 3) Four F_2 population
vii.	**Package of practices**	**:**	As per recommendations
viii.	**Genotypes to be used in research**	**:**	SKP 84 ANDCP-16-1 JP 105 JP 107 JI 456

13.2 Observations to be recorded

The following procedure will be adopted to record varioos morphological and quantitative characters:

13.2.1 Morphological characters

The morphological characters will be recorded according to the DUS guidelines. The observations will be recorded on five individual plant of parents, F_{1s} and 50 plants of F_2 population. The detail procedure adopted for recording various morphological characters will be as follows:

13.2.1.1	**Types of internode**	**:**	1. Condensed 2. Elongated
13.2.1.2	**Leaf shape**	**:**	1. Flat 2. Shallow cup 3. Deep cup
13.2.1.3	**Inflorescence shape**	**:**	1. Umbrella 2. Cylindrical 3. Conical
13.2.1.4	**Inflorescence compactness**	**:**	1. Loose 2. Semi-compact 3. Compact
13.2.1.5	**Branching pattern**	**:**	1. Convergent

2. Divergent

13.2.1.6 Location of branches **:**
1. Top
2. Basal
3. All over

13.2.1.7 Capsule spininess **:**
1. Absent
2. Sparse
3. Dense

13.2.1.8 Seed shape **:**
1. Elongated
2. Oval
3. Square

13.2.1.9 Seed coat colour **:**
1. White
2. Maroon
3. Light brown
4. Dark brown
5. Black

13.2.2 Quantitative characters

The observations will be recorded on five plants of parents and F_1 and 50 plants of F_2 generation. The method used for data collection of individual character is described below.

13.2.2.1 Days to flowering of primary raceme

The number of days from the date of sowing to the appearance of flowers on the primary raceme of selected plants will be recorded.

13.2.2.2 Days to maturity of primary raceme

The number of days from the date of sowing to the physiological maturity of the primary raceme of selected plants will be recorded.

13.2.2.3 Number of nodes up to primary raceme

The total number of nodes from the cotyledonary node to the base of primary raceme will be counted at the time of maturity.

13.2.2.4 Number of capsules on primary raceme

The total number of capsules born on primary raceme will be counted at the time of maturity.

13.2.2.5 Plant height up to primary raceme (cm)

The height of the plant will be measured from the base of the plant to the base of the primary raceme in centimeters at maturity.

13.2.2.6 Effective length of primary raceme (cm)

The length of capsule bearing part of the primary raceme will be measured in centimeters at the time of maturity.

13.2.2.7 Number of effective branches per plant

The number of raceme-bearing branches will be considered as effective

branches and it will be counted at the time of maturity.

13.2.2.8 Shelling out turn (%)

Well mixed 100 g capsules of each plant will be manually threshed and shelling out turn will be calculated as per following formula.

$$\text{Shelling out turn (\%)} = \frac{\text{Seed weight (g)}}{\text{Capsule weight (g)}} \times 100$$

13.2.2.9 Seed yield per plant (g)

All the effective racemes per plant will be threshed together and cleaned-dried seeds will be weighed in grams.

13.2.2.10 Oil content (%)

A random sample of dried seeds will be taken from each plant individually and oil content will be determined in percentage by using Nuclear Magnetic Resonance Technique (Tiwari *et al.*, 1974).

13.2.2.11 Sex expression in primary raceme

The individual selected plants will be counted for pistillate, monoecious and intersperse nature in primary raceme.

13.2.2.12 Sex expression in secondary raceme

The individual selected plants will be counted for pistillate, monoecious and intersperse nature in secondary raceme separately.

13.2.2.13 Sex expression in tertiary raceme

The individual selected plants will be counted for pistillate, monoecious and intersperse nature in tertiary raceme separately.

14. Statistical Analysis

The data generated for the various characters in each plant of F_2 generation will be used for statistical analysis.

14.1 Analysis of variance

Analysis of variance technique described by Panse and Sukhatme (1985) will be followed to test the differences among the individuals for all the characters.

14.2 Morphological and sex expression analysis

Genetics of morphological and sex expression analysis will be studied and the significance of differences between observed and expected frequencies or ratio for qualitative characters will be tested by using Karl Pearson's Chi-square test (χ^2 test).

The general formula of χ^2 test was as follows:

$$\chi^2 = \frac{\sum(O - E)^2}{E}$$

Where,

Σ = Summation,

O = Observed frequencies and

E = Expected frequencies

14.3 Variability parameters

The variability parameters *viz*., genotypic coefficient of variance, phenotypic coefficient of variance, heritability and genetic advance will be estimated as per method suggested by Burton (1952) and Allard (1960).

14.4 Correlation analysis

The estimates of covariance will be calculated according to the Singh and Chaudhary (1985). The genotypic and phenotypic correlations will be worked out following the procedure suggested by Al-Jibouri *et al*. (1958).

14.5 Path analysis

Path coefficient analysis will be carried out on the basis of correlation to find out the direct and indirect effects of variables as per the procedure suggested by Wright (1921) and reviewed by Dewey and Lu (1959).

15. References

Ahmed, H. M., Sarwar, G. and Muhammad, A. (2012). Genetic variability and interdependence of morphological traits in castor bean (*Ricinus communis* L.) mutants. *Songklanakarin Journal of Science and Technology*, **34(3):** 279-286.

Alemaw, G., Beemnet, M. K., Girma, T. and Chalachew, E. (2014). Phenotypic variability in Ethiopian castor (*Ricinus communis* L.) accessions. *International Journal of Advanced Biology and Biomedical Research,* **2(12):** 2909-2914.

Alhaji, K. A., Oliseh, A., Salihu, B. Z. and Kabaraini, M. A. (2019). Studies on genetic variability and trait relationship in castor (*Ricinus communis* L.). *Journal of Plant Development,* **26:** 3-11.

Al-Jibouri, H. A., Miller, P. A. and Robinson, H. F. (1958). Genotypic and environmental variances in upland cotton cross of interspecific origin. *Journal of Agronomy,* **50:** 633-635.

Allard, R. W. (1960). *Principle of Plant Breeding*. John Willey and Sons, Inc., New York. pp. 83-88.

Anjani, K. (2012). Castor genetic resources: A primary gene pool for exploitation. *Industrial Crops and Products,* **35:** 1-14.

Anjani, K. and Sridevi, O. (2016). Castor breeding in India-Current status and future prospects. *Indian Journal of Genetics and Plant Breeding*, **76(4):** 583–597.

Ankineedu, G. and Rao, G. P. (1973). Development of pistillate castor. *Indian Journal of Genetics and Plant Breeding*, **33:** 416-422.

Anonymous (2024a). Area, Production and Productivity of castor of India 2024-25. Available at https://commodities.cmie.com. Accessed on 15th Dec., 2025.

Anonymous (2024b). Area, Production and Productivity 2024-25, Final advanced estimates, Directorate of Agriculture, Government of Gujarat, Gandhinagar. Available at https://www.dag.gujarat.gov.in. Accessed on 15th Dec., 2025.

Bhat, N. U., Sadaiah, K., Ramya, K. T., Anuradha, C. and Manjunatha, T. (2025). Evaluation of agronomic traits and genetic relationships among elite breeding lines of castor (*Ricinus communis* L.). *Journal of Experimental Agriculture International,* **47(7):** 594-606.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proc. 6th International Grassland Congress,* **1:** 277-283.

Chaitanya, S. K., Venkateswarlu, O., Sekhar, M. R. and Reddy, B. V. B. (2013). Character association and path analysis among yield components in castor (*Ricinus communis* L.). *Journal of Oilseeds Research*, **30(1):** 74-76.

Chaudhari, B. A., Patel, M. P., Patel, J. A., Makwana, R. R., Patel A. M. and Patel, M. K. (2019). The characterization of castor (*Ricinus communis* L.) genotypes for morphological traits. *International Journal of Current Microbiology and applied Sciences*, **8(05):** 2482-2492.

Chaudhari, D. R., Parmar, V. L., Dube, D. V., Bhakta, R. S., Patel, A. I. and Lodam, V. A. (2016). Genetic variability and divergence study in castor (*Ricinus Communis* L.). *Advances in Life Sciences*, **5(16):** 6418-642.

Classen, C. E. and Hoffman, A. (1950). The inheritance of the pistillate character in castor and its possible utilization in the production of commercial hybrid seed, *Journal of Agronomy*, **42:** 79-82.

Dapke, J. S., Naik, M. R., Singh, A. P., Baraskar, V. V., Narwade, A. V. and Indivar, P. (2016). Genetic association yield with different agronomic traits in castor (*Ricinus communis* L.). *International Journal of Biology Research*, **1(1):** 47-49.

Deepak, K. A., Manjunatha, T., Hemalatha, V. and Chary, D. S. (2024). Variability, correlation patterns and principal component analysis (PCA) for seed yield and contributing traits in castor (*Ricinus communis* L.). *Journal of Advances in Biology and Biotechnology*, **27(8):** 1217-1227.

Deepika, C., Venkatachalam, S. R., Yuvaraja, A., Arutchenthil, P., Indra, N., Ravichandran, V., Veeramani, P. and Kathirvelan, P. (2022). Morphometric description and genetic diversity in 208 monoecious and pistillate castor (*Ricinus communis* L.) genotypes: an unexplored industrial oil crop in semi-arid tropics. *Euphytica*, **218(11):** 163.

Deepika, C., Venkatachalam, S. R., Yuvaraja, A., Arutchenthil, P., Indra, N., Ravichandran, V., Veeramani, P. and Kathirvelan, P. (2025). Deciphering heterotic potential and pistillate character expression in castor (*Ricinus communis* L.). *Agricultural Research*, pp. 1-9.

Dewey, D. R. and Lu, K. H. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, **51(9):** 515-518.

Dhedhi, K. K., Ghelani, Y. H., Joshi, H. J. and Dangaria, C. J. (2010). Correlation and path coefficient analysis in castor (*Ricinus communis* L.) over environments. *Agricultural Science Digest,* **30(4):** 286-289.

FAOSTAT, (2023). Area, production and productivity of castor oil seed. Food and Agriculture Organization of the United Nations. Available at: https://www.fao.org/faostat/.in. Accessed on 5th August, 2023.

Fisher, R. A. (1918). *The Correlation Among Relatives on the Supposition of Mendelian Inheritance*. Trans, Royal Soc., Edinburgh, **52:** 399-433.

Galton, F. (1889). *Natural Inheritance*. Mc Millan, London Publisher.

Gogoi, S. N., Chakravotry, R. and Barua, P. K. (2009). Correlation and path analysis in local castor genotypes, the host plant of eri silkworm (*Samiaricini donovan*). *Advances Plant Sciences*, **22(1):** 277-279.

Gopani, D. D., Kabaria, M. M. and Patel, R. H. (1969). Study of sex reversion in castor. *Indian Journal of Agricultural Sciences,* **39:** 255-258.

Johansen, W. (1909). *Elements der exatetenexbiblchkeitslehrajena*. *Gustan Fisher*, pp: 20.

Johnson, H. W., Robinson, H. F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, **47(7):** 314-318.

Kote, U. B., Rao, S. V. and Rao, S. M. (2013). Genetic variability in castor (*Ricinus communis* L.) for yield and its contributing traits**.** *International Journal of Food, Agriculture and Veterinary Sciences,* **3**(**3):** 103-108.

Kulkarni, L. G. (1959). Castor, Hyderabad: Indian Central Oilseeds Committee, Hyderabad., pp: 8-35.

Lakshmamma, P., Lakshmi, P., Mohan, Y. C. and Lavanya, C. (2005). Genetic variability and character association in castor (*Ricinus communis* L.). *National Journal of Plant Improvement,* **7(2)**: 122-126.

Lavanya, C. (2002). Sensitivity of sex expression and sex variation in castor (*Ricinus communis* L.) to environmental changes. *Indian Journal of Genetics and Plant Breeding*, **62(3):** 232-237.

Lavanya, C. and Gopinath, V. (2008). Inheritance studies for morphological characters and sex expression in pistillate lines of castor (*Ricinus communis* L). *Indian Journal of Genetics and Plant Breeding*, **68(3):** 275-282.

Lavanya, C., Manjunatha, T., Senthilvel, S. and Ramya, K. T. (2022). Genetic variability studies of major yield components in segregating population derived from pistillate lines of castor (*Ricinus communis* L.). *Journal of Oilseeds Research,* **39(3):** 174-178.

Manjunatha, T., Ramya, K. T., Lavanya, C., Sarada, C. Senthilvel, S., Yamanura, M., Patel, C. J., Patel, A. M., Patel, M., Madariya, R. and Yadav, P. (2023). Genetic nature and role of environment in sex expression and phenological characters of pistillate lines in castor (*Ricinus communis* L.). *Genetic Resources and Crop Evolution,* **71:** 2617-2630.

Movaliya, H. M., Chovatia, V. P., Madariya, R. B., Mungala, R. A., Pipaliya, H. R. and Bhuva, S. K. (2018). Study of variability and correlation for seed yield and its attributes in castor (*Ricinus communis* L). *Journal of Pharmacognosy and Phytochemistry*, **7(2):** 1474-1477.

Mullualem, D., Alemaw, G., Petros, Y. and Alemu, S. (2017). Phenotypic variability and association of traits among yield and yield-related traits in castor (*Ricinus communis* L.) accessions at Melkassa, Central Rift Valley of Ethiopia. *African Journal of Agricultural Research,* **12(52):** 3562-3568.

Muppala, P., Reddy, T. P. and Sujatha, M. (2018*).* Industrial importance and utilization of castor oil and its derivatives. *Current Science,* **114(12):** 2437-2443.

Mutlu, H. and Meier, M. A. R. (2010). Castor oil as a renewable resource for the chemical industry. *European Journal of Lipid Science and Technology*, **112(1):** 10-30.

Nilsson Ehle, H. (1909). *Kreuzungs-untersuchungen an Hafer und Weizen*, in *Acta Universitatis lundensis*, **2:** 1-122.

Panera, A., Jalu, R. K. and Virani, H. B. (2018) Inheritance of *Fusarium* wilt resistance and certain morphological characters in castor (*Ricinus communis* L.). *Bulletin of Environment, Pharmacology and Life Sciences,* **7(12):** 30-35.

Panse, V. G. and Sukhatme, P. V. (1985). *Statistical Methods for Agricultural Workers*, ICAR, New Delhi.

Patel, C. M., Patel, J. M., Gami, R. A. and Patel, C. J. (2014). Inheritance studies on sex expression under varying environments in castor (*Ricinus communis* L.). *International Journal of Plant, Animal and Environmental Sciences,* **4(3):** 611-614.

Patel, D. K., Ravindrababu, Y. and Prajapati, D. B. (2011). Variability and character association analysis in castor (*Ricinus communis* L.). *International Journal of Plant Sciences,* **6(2):** 292-295.

Patel, I. D., Dangaria, C. J. and Patel, V. J. (1986). Induction of male sex in pistillateness of castor. *Indian Journal of Agricultural Science*, **56(8):** 556-558.

Patel, J. K. and Nakarani, D. B. (2016). Character association and path analysis in castor (*Ricinus communis* L.). *International Journal of Agricultural Science.*, **12(1):** 22-27.

Patel, J. K. and Patel, P. C. (2014). Genetic variability, heritability and genetic advance for yield and yield components in castor (*Ricinus communis* L.) genotypes. *International Journal of Plant Science*, **9(2):** 385-388.

Patel, J. R., Saiyed, M. P., Patel, C. G. Bhatt, R. K. and Bhatt, J. P. (2010). Genetic variability and correlation studies in castor (*Ricinus communis* L.). *International Journal of Agricultural Science*, **6(1):** 129-131.

Patel, P. D., Chaudhari, K. N. and Patel, D. A. (2016). Inheritance study of some morphological traits in castor (*Ricinus communis* L.). *Advances in Life Sciences* **5(3):** 773-776.

Patel, R. H., Patel, D.M. and Patel, B. N. (2019). Trends in castor production and productivity in Gujarat state-An overview. *Gujarat Agricultural University Research Journal*, **44(2):** 56-62.

Ramesh, M., Lavanya, C., Sujatha, M., Bhave, M. H. V. and Aruna, J. (2017). Inheritance of morphological characters and sex expression in castor (*Ricinus communis* L.). *Journal of Oilseeds Research*, **34(4):** 247-250.

Rana, M., Dhamija, H., Prashar, B. and Sharma, S. (2012). *Ricinus communis* L. A review. *International Journal of Pharm Tech Research*, **4(4):** 1706-1711.

Rao, K. V., Reddy, V. R. K. and Anjani, K. (2011). Genetic diversity and germplasm utilization in castor. *Journal of Oilseeds Research*, **28(Special Issue):** 61-67.

Rao, S. M., Bhanu, U. K., Rao, S. V. and Ahamed, L. M. (2014). The characterization of castor *(Ricinus communis* L.) germplasm for morphological traits. *International Journal of Development Research*, **4(5):** 1125-1128.

Reddy, P. S., Priya, P. B., Sadaiah, K., Vanisri, S. and Kumar, C. S. (2022). Genetic variability and character association studies among yield attributing traits in genepool lines of castor (*Ricinus communis* L.). *Biological Forum-An International Journal*, **14(2):** 1277-1281.

Rukhsar, S., Patel, M. P., Parmar, D. J. and Kumar, S. (2018). Genetic variability, character association and genetic divergence studies in castor (*Ricinus communis* L.). *Annals of Agrarian Science*, **16:** 143-148.

Sadaiah, K., Neelima, G., Madhuri, G., Rani, V. D., Nalini, N., Shankar, V. G., Kumar, M. P., Sujatha, M. and Goverdhan, M. (2023). Gene action, combining ability, genetic parameters and character association studies in castor (*Ricinus communis* L.). *Environment and Ecology*, **41 (1B):** 496-503.

Sadaiah, K., Neelima, G., Rani, C. V. D., Rani, V. D., Madhuri, G., Nalini, N., Sujatha, M., Shankar, V. G., Parimal, M., Lavanya, C., Jawahar, J. and Raju, C. D. (2021). Genetic parameters, diversity and character association studies in germplasm lines of castor (*Ricinus communis* L.). *Electronic Journal of Plant Breeding*, **12(4):** 1134-1141.

Sailaja, M. and Anjani, K. (2015). Utilization of castor cake as organic manure after detoxification. *Indian Journal of Agricultural Sciences*, **85(9):** 1189-1192.

Severino, L. S., Auld, D. L., Baldanzi, M., Candido, M. J. D., Chen, G., Crosby, W., Tan, D., Xiaohua, H., Lakshmamma, P., Lavanya, C., Machado, O. L. T., Thomas, M., Milani, M., Miller, T. D., Morris, J. B., Morse, S. A., Navas, A. A., Soares, D. J., Sofiatti, V., Wang, M. L., Zanotto, M. D. and Zieler, H. (2012). A review on the challenges for increased production of castor. *Journal of Agronomy*, **4(4):** 853-880.

Sevugaperumal, S., Rangasamy, P. and Muppidathi, N. (2000). Genetic variability, correlation and path coefficient analysis in castor (*Ricinus communis* L.). *Madras Agricultural Journal*, **86(7/9):** 456-459.

Shankar, V. G., Rao, V. R. and Reddy, A. V. (2010). Inheritance of certain morphological characters and *Fusarium* wilt resistance in castor (*Ricinus communis* L.). SABRAO *Journal of Breeding and Genetics*, **42(2):** 57-64.

Shifriss, O. (1960). Conventional and unconventional systems controlling sex variations in *Ricinus*. *Journal of Genetics*, **57:** 573-578.

Singh, D. (1976). Castor-*Ricinus communis* (Euphorbiaceae). In: Simmonds NW (ed.) Evolution of Crop Plants, Longman, London. pp. 84-86.

Singh, R. K. and Chaudhary, B. D. (1985). *Biometrical methods in quantitative genetics analysis*. Kalyani Publishers, Ludhiana and Delhi, pp**.** 262-282.

Solanki, S. S. and Joshi, P. (2001). Inheritance study of some morphological traits in castor (*Ricinus communis* L.). *Indian Journal of Genetics and Plant Breeding.*, **61(2):** 136-139.

Sowmya, P., Vanaja, M., Sunitha, V., Anitha, Y. and Kumar Vijay, Y. (2015). Variability and correlation studies for seed yield and yield contributing components of castor (*Ricinus communis* L.) germplasm under rainfed conditions. *International Journal of Current Science,* **15:** 59-65.

Sowmya, P., Vanaja, M., Sunita, V. and Reddy, P. R. (2019). Variability and genetic advance for seed yield and its components in castor (*Ricinus communis* L.) germplasm of CRIDA under rain-fed conditions in alfisols. *International Journal of Current Microbiology and Applied Sciences,* **8(1):** 2001-2011.

Sridhar, V., Dangi, R. A. V., Sudhakar, R. and Sankar, A. S. (2009). Genetic variability in F_2 populations of castor (*Ricinus communis* L.). *International Journal of Agriculture Environment and Biotechnology,* **2(3):** 227-229.

Tewari, N. and Mishra, A. (2013). Correlation and path coefficient analysis of castor (*Ricinus communis* L.) in non-traditional area of central Uttar Pradesh. *International Journal of Genetic Engineering and Biotechnology*, **4(1):** 1-9.

Tiwari, P. N., Gambhir, P. M. and Rajan, T. S. (1974). Rapid and nondestructive determination of seed oil by pulsed nuclear magnetic resonance technique. *Journal of American Oil Chemists Society*, **51:** 104-109.

Venkatachalam, S. R., Nagarajan, S., Viswanathn, P. L., Manickam, S. and Ganpathi, N. (2019). Correlation and path coefficient analysis in castor (*Ricinus communis* L.). *International Journal of Pure and Applied Biosciences*, **7(3):** 230-233.

Weiss, E. A. (2000). *Oilseed Crops*, Oxford, Blackwell Science. pp. 364.

Wright, S. (1921). The methods of the path coefficients. *Ann. Math. Stat.*, **5(3):** 161-215.

Yadava, D. K., Vasudev, S., Singh, N., Mohapatra, T. and Prabhu, K. V. (2012). *Breeding Major Oil Crops: Present Status and Future Research Needs.* In: Gupta, S. K. (ed.), *Technological Innovation in Major World Oil Crops*, Vol. 1: Breeding Springer Science + Business Media, LLC, Berlin, Germany, p. 17.

Yamanura, R. and Kumar, R. M. (2020). Study of genetic variability, path coefficient and genetic diversity in castor (*Ricinus communis* L.). *The Pharma Innovation Journal,* **9(8):** 285-292.

Yamanura, R., Kumar, R. M., Sangannavar, P. A. and Boraiah, B. (2024). Exploring agro-morphological variation, genetic diversity and trait associations in castor (*Ricinus communis* L.) genotypes. *Electronic Journal of Plant Breeding*, **15(2):** 487-495.

Zimmerman, L. H. and Smith, J. D. (1966). Production of F_1 seed in castor bean by use of sex genes sensitive to environment. *Crop Science*, **6:** 406-409.

Sign. of Student **Sign. of Major Guide**

(Kapadiya Avani P.) **(Dr. R. B. Madariya)**